

5'-tag gtg gtg tca ttc ccc tcc aac ctg agt gct ggc agg tac act gct	48
ggc cac cag cag atg ccc atg aag atg ctg aca atg aag atg ctg gcc	96
Met Pro Met Lys Met Leu Thr Met Lys Met Leu Ala	12
ctg tgc ttg gtt ctt gct aaa tca gcc tgg tgc gag gaa cag gag aag	144
Leu Cys Leu Val Leu Ala Lys Ser Ala Trp Ser Glu Glu Gln Glu Lys	28
gtg gtt cat gga ggc ccg tgt ttg aag gac tcc cac cct ttc cag gct	192
Val Val His Gly Gly Pro Cys Leu Lys Asp Ser His Pro Phe Gln Ala	44
gcc ctc tac acc tca ggt cac ttg ctg tgt ggt ggg gtc ctc att gac	240
Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly Gly Val Leu Ile Asp	60
cca cag tgg gtg ctg aca gct gcc cac tgc aaa aaa ccg aat ctg cag	288
Pro Gln Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln	76
gtg atc ttg ggg aaa cac aac cta cgg caa aca gag act ttc caa agg	336
Val Ile Leu Gly Lys His Asn Leu Arg Gln Thr Glu Thr Phe Gln Arg	92
caa atc tca gtg gac agg act att gtc cat ccc cgc tac aac cct gaa	384
Gln Ile Ser Val Asp Arg Thr Ile Val His Pro Arg Tyr Asn Pro Glu	108
acc cac gac aat gac atc atg atg gtg cat ctg aaa aat cca gtc aaa	432
Thr His Asp Asn Asp Ile Met Met Val His Leu Lys Asn Pro Val Lys	124
ttc tct aaa aag atc cag cct ctg ccc ttg aag aat gac tgc tct gag	480
Phe Ser Lys Lys Ile Gln Pro Leu Pro Leu Lys Asn Asp Cys Ser Glu	140
gag aat ccc aac tgc cag atc ctg ggc tgg ggc aag atg gaa aat ggt	528
Glu Asn Pro Asn Cys Gln Ile Leu Gly Trp Gly Lys Met Glu Asn Gly	156
gac ttc cca gat acc att cag tgt gct gat gtc cat ctg gtg ccc cgg	576
Asp Phe Pro Asp Thr Ile Gln Cys Ala Asp Val His Leu Val Pro Arg	172
gag cag tgt gag cgt gcc tac cct ggc aag atc acc cag agc atg gtg	624
Glu Gln Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Gln Ser Met Val	188
tgc gca ggc gac atg aaa gaa ggc aac gat tcc tgt cag ggt gat tct	672
Cys Ala Gly Asp Met Lys Glu Gly Asn Asp Ser Cys Gln Gly Asp Ser	204

FIGURE 1A.

gga ggt ccc cta gta tgt ggg ggt cgc ctc cga ggg ctc gtg tca tgg	720
Gly Gly Pro Leu Val Cys Gly Gly Arg Leu Arg Gly Leu Val Ser Trp	220

ggt gac atg ccc tgt gga tca aag gag aag cca gga gtt tac acc gat	768
Gly Asp Met Pro Cys Gly Ser Lys Glu Lys Pro Gly Val Tyr Thr Asp	236

gtc tgc act cat atc aga tgg atc caa aac atc ctc aga aac aag tgg	816
Val Cys Thr His Ile Arg Trp Ile Gln Asn Ile Leu Arg Asn Lys Trp	252

ctg tga-3'	822
Leu	253

FIGURE 1B